SEQUENCE LISTING

<110> Kennedy, Giulia
Kang, Sanmao
Reinhard, Christoph
Jefferson, Anne Bennett

<120> POLYNUCLEOTIDES RELATED TO COLON CANCER

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<141> 2001-06-14

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<151> 2000-06-15

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cat gtg cgg ggg gtg ggg tcc cgt ggc ttc ccc ctg cgc ctc cag gcc
101
His Val Arg Gly Val Gly Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala
15 20 25

acc gag gtc cgt atc tgc cct gtg gaa ttc aac ccc aac ttc gtg gcg
149
Thr Glu Val Arg Ile Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala
30 35 40

cgt atg ata cct aaa gtg gag tgg tcg gcg ttc ctg gag gcg gcc gat
197
Arg Met Ile Pro Lys Val Glu Trp Ser Ala Phe Leu Glu Ala Ala Asp
45 50 55

aac ttg cgt ctg atc cag gtg ccg aaa ggg ccg gtt gag gga tat gag
245
Asn Leu Arg Leu Ile Gln Val Pro Lys Gly Pro Val Glu Gly Tyr Glu
60 65 70 75

gag aat gag gag ttt ctg agg acc atg cac cac ctg ctg ctg gag gtg
293
Glu Asn Glu Glu Phe Leu Arg Thr Met His His Leu Leu Leu Glu Val
80 85 90

gaa gtg ata gag ggc acc ctg cag tgc ccg gaa tct gga cgt atg ttc
341
Glu Val Ile Glu Gly Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe
95 100 105

ccc atc agc cgc ggg atc ccc aac atg ctg ctg agt gaa gag gaa act
389
Pro Ile Ser Arg Gly Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr
110 115 120

gag agt t gattgtgcca ggcgccagtt tttcttgtta tgactgtgta tttttgttga
446
Glu Ser
125

tctataccct gtttccgaat tctgccgtgt gtatccccaa cccttgaccc aatgacacca
506
aacacagtgt ttttgagctc ggtattatat atttttttct cattaaaggt ttaaaacc
564

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20 25 30
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35 40 45
Val Glu Trp Ser Ala Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile
50 55 60
Gln Val Pro Lys Gly Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe
65 70 75 80
Leu Arg Thr Met His His Leu Leu Leu Glu Val Glu Val Ile Glu Gly
85 90 95
Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe Pro Ile Ser Arg Gly
100 105 110
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120
tgctagggcc agcctgcgca ttcttacctg tcggggtgcg gcgagtgtct cacctctctg
180
cacttccaag gactcttgtc atctgcctta ggcgggaa atg ctg ttg ctg gat tgc
236
Met Leu Leu Leu Asp Cys
1 5

aac ccc gag gtg gat ggt ctg aag cat ttg ctg gag aca ggg gcc tcg
284
Asn Pro Glu Val Asp Gly Leu Lys His Leu Leu Glu Thr Gly Ala Ser
10 15 20

gtc aac gca ccc ccg gat ccc tgc aag cag tcg cct gtc cac tta gcc
332
Val Asn Ala Pro Pro Asp Pro Cys Lys Gln Ser Pro Val His Leu Ala
25 30 35

gca gga agc ggc ctt gct tgc ttt ctt ctc tgg cag ctg caa acg ggc
380
Ala Gly Ser Gly Leu Ala Cys Phe Leu Leu Trp Gln Leu Gln Thr Gly
40 45 50

gct gac ctc aac cag cag gat gtt tta gga gaa gct cca cta cac aag
428
Ala Asp Leu Asn Gln Gln Asp Val Leu Gly Glu Ala Pro Leu His Lys
55 60 65 70

gca gca aaa gtt gga agc ctg gag tgc cta agc ctg ctt gta gcc agt
476
Ala Ala Lys Val Gly Ser Leu Glu Cys Leu Ser Leu Leu Val Ala Ser
75 80 85

gat gcc caa att gat tta tgt aat aag aac ggg caa aca gct gaa gat
524
Asp Ala Gln Ile Asp Leu Cys Asn Lys Asn Gly Gln Thr Ala Glu Asp
90 95 100

ctc gct tgg tca tgt gga ttt cca gac tgt gcc aag ttt ctt aca aca
572
Leu Ala Trp Ser Cys Gly Phe Pro Asp Cys Ala Lys Phe Leu Thr Thr
105 110 115

att aaa tgt atg cag aca ata aaa gca agt gaa cac cct gac agg aat
620
Ile Lys Cys Met Gln Thr Ile Lys Ala Ser Glu His Pro Asp Arg Asn
120 125 130

gat tgt gtt gcc gtg ctc aga cag aaa cgg agt ctc gga agt gta gaa
668
Asp Cys Val Ala Val Leu Arg Gln Lys Arg Ser Leu Gly Ser Val Glu
135 140 145 150

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713
Asn Thr Ser Gly Lys Arg Lys Cys
155

gaagtctgaa gaacgccttc atttcatgca aatctataag ctcctgcttt tggctttacc
773
atatgttgtg tctaatctcc ttctgagaag gacgaaaaac tttcttccaa gtgaagatcc
833
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919

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Ser Pro Val His Leu Ala Ala Gly Ser Gly Leu Ala Cys Phe Leu Leu
        35   40   45
Trp Gln Leu Gln Thr Gly Ala Asp Leu Asn Gln Gln Asp Val Leu Gly
    50   55   60
Glu Ala Pro Leu His Lys Ala Ala Lys Val Gly Ser Leu Glu Cys Leu
65   70   75   80
Ser Leu Leu Val Ala Ser Asp Ala Gln Ile Asp Leu Cys Asn Lys Asn
                85   90   95
Gly Gln Thr Ala Glu Asp Leu Ala Trp Ser Cys Gly Phe Pro Asp Cys
            100   105   110
Ala Lys Phe Leu Thr Thr Ile Lys Cys Met Gln Thr Ile Lys Ala Ser
        115   120   125
Glu His Pro Asp Arg Asn Asp Cys Val Ala Val Leu Arg Gln Lys Arg
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Ser Leu Gly Ser Val Glu Asn Thr Ser Gly Lys Arg Lys Cys
145   150   155
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ctg tac atg gtg aat gga cca cca cat ttt aca gaa agc aca gtg ttt
97

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Leu Tyr Met Val Asn Gly Pro Pro His Phe Thr Glu Ser Thr Val Phe
                  20                  25                  30

cca agg gaa tct ggg aag aat tgc aaa gtc tgt atc ttt agt aag gat
145
Pro Arg Glu Ser Gly Lys Asn Cys Lys Val Cys Ile Phe Ser Lys Asp
             35                  40                  45

ggg acc ttg ttt gcc tgg ggc aat gga gaa aaa gta aat att atc agt
193
Gly Thr Leu Phe Ala Trp Gly Asn Gly Glu Lys Val Asn Ile Ile Ser
         50                  55                  60

gtc act aac aag gga cta ctg cac tcc ttc gac ctc ctg aag gca gtt
241
Val Thr Asn Lys Gly Leu Leu His Ser Phe Asp Leu Leu Lys Ala Val
     65                  70                  75

tgc ctt gaa ttc tca ccc aaa aat act gtc ctg gca acg tgg cag cct
289
Cys Leu Glu Phe Ser Pro Lys Asn Thr Val Leu Ala Thr Trp Gln Pro
 80                  85                  90                  95

tac act act tct aaa gat ggc aca gct ggg ata ccc aac cta caa ctt
337
Tyr Thr Thr Ser Lys Asp Gly Thr Ala Gly Ile Pro Asn Leu Gln Leu
                 100                 105                 110

tat gat gtg aaa act ggg aca tgt ttg aaa tct ttc atc cag aaa aaa
385
Tyr Asp Val Lys Thr Gly Thr Cys Leu Lys Ser Phe Ile Gln Lys Lys
             115                 120                 125

atg caa aat tgg tgt cca tcc tgg tca gaa gat gaa act ctt tgt gcc
433
Met Gln Asn Trp Cys Pro Ser Trp Ser Glu Asp Glu Thr Leu Cys Ala
         130                 135                 140

cgc aat gtt aac aat gaa gtt cac ttc ttt gaa aac aac aat ttt aac
481
Arg Asn Val Asn Asn Glu Val His Phe Phe Glu Asn Asn Asn Phe Asn
     145                 150                 155

aca att gca aat aaa ttg cat ttg caa aaa att aat gac ttt gta tta
529
Thr Ile Ala Asn Lys Leu His Leu Gln Lys Ile Asn Asp Phe Val Leu
160                 165                 170                 175

tca cct gga ccc caa cca tac aag gtg gct gtc tat gtt cca gga agt
577
Ser Pro Gly Pro Gln Pro Tyr Lys Val Ala Val Tyr Val Pro Gly Ser
                 180                 185                 190

aaa ggt gca cct tca ttt gtt aga tta tat cag tac ccc aac ttt gct
625
Lys Gly Ala Pro Ser Phe Val Arg Leu Tyr Gln Tyr Pro Asn Phe Ala
             195                 200                 205
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673
Gly Pro His Ala Ala Leu Ala Asn Lys Ser Phe Phe Lys Ala Asp Lys
        210                 215                 220

gtt aca atg ctg tgg aat aaa aaa gct act gct gtg ttg gta ata gct
721
Val Thr Met Leu Trp Asn Lys Lys Ala Thr Ala Val Leu Val Ile Ala
    225                 230                 235

agc aca gat gtt gac aag aca gga gct tcc tac tat gga gaa caa act
769
Ser Thr Asp Val Asp Lys Thr Gly Ala Ser Tyr Tyr Gly Glu Gln Thr
240                 245                 250                 255

cta cac tac att gca aca aat gga gaa agt gct gta gtg caa tta cca
817
Leu His Tyr Ile Ala Thr Asn Gly Glu Ser Ala Val Val Gln Leu Pro
                260                 265                 270

aaa aat ggc ccc att tat gat gta gtt tgg aat tct agt tct act gag
865
Lys Asn Gly Pro Ile Tyr Asp Val Val Trp Asn Ser Ser Ser Thr Glu
            275                 280                 285

ttt tgt gct gta tat ggt ttt atg cct gcc aaa gcg aca att ttc aac
913
Phe Cys Ala Val Tyr Gly Phe Met Pro Ala Lys Ala Thr Ile Phe Asn
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ttg aaa tgt gat cct gta ttt gac ttt gga act ggt cct cgt aat gca
961
Leu Lys Cys Asp Pro Val Phe Asp Phe Gly Thr Gly Pro Arg Asn Ala
    305                 310                 315

gcc tac tat agc cct cat gga cat ata tta gta tta gct gga ttt gga
1009
Ala Tyr Tyr Ser Pro His Gly His Ile Leu Val Leu Ala Gly Phe Gly
320                 325                 330                 335

aat ctg agg gga caa atg gaa gtg tgg gat gtg aaa aac tac aaa ctt
1057
Asn Leu Arg Gly Gln Met Glu Val Trp Asp Val Lys Asn Tyr Lys Leu
                340                 345                 350

att tct aaa ccg gtg gct tct gat tct aca tat ttt gct tgg tgc ccg
1105
Ile Ser Lys Pro Val Ala Ser Asp Ser Thr Tyr Phe Ala Trp Cys Pro
            355                 360                 365

gat ggt gag cat att tta aca gct aca tgt gct ccc agg tta cgg gtt
1153
Asp Gly Glu His Ile Leu Thr Ala Thr Cys Ala Pro Arg Leu Arg Val
        370                 375                 380
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aat aat gga tac aaa att tgg cat tat act ggc tct atc ttg cac aag
1201
Asn Asn Gly Tyr Lys Ile Trp His Tyr Thr Gly Ser Ile Leu His Lys
385 390 395

tat gat gtg cca tca aat gca gaa tta tgg cag gtt tct tgg cag cca
1249
Tyr Asp Val Pro Ser Asn Ala Glu Leu Trp Gln Val Ser Trp Gln Pro
400 405 410 415

ttt ttg gat gga ata ttt cca gca aaa aca ata act tac caa gca gtt
1297
Phe Leu Asp Gly Ile Phe Pro Ala Lys Thr Ile Thr Tyr Gln Ala Val
420 425 430

cca agt gaa gta ccc aat gag gaa cct aaa gtt gca aca gct tat aga
1345
Pro Ser Glu Val Pro Asn Glu Glu Pro Lys Val Ala Thr Ala Tyr Arg
435 440 445

ccc cca gct tta aga aat aaa cca atc acc aat tcc aaa ttg cat gaa
1393
Pro Pro Ala Leu Arg Asn Lys Pro Ile Thr Asn Ser Lys Leu His Glu
450 455 460

gag gaa cca cct cag aat atg aaa cca caa tca gga aac gat aag cca
1441
Glu Glu Pro Pro Gln Asn Met Lys Pro Gln Ser Gly Asn Asp Lys Pro
465 470 475

tta tca aaa aca gct ctt aaa aat caa agg aag cat gaa gct aag aaa
1489
Leu Ser Lys Thr Ala Leu Lys Asn Gln Arg Lys His Glu Ala Lys Lys
480 485 490 495

gct gca aag cag gaa gca aga agt gac aag agt cca gat ttg gca cct
1537
Ala Ala Lys Gln Glu Ala Arg Ser Asp Lys Ser Pro Asp Leu Ala Pro
500 505 510

act cct gcc cca cag agc aca cca cga aac act gtc tct cag tca att
1585
Thr Pro Ala Pro Gln Ser Thr Pro Arg Asn Thr Val Ser Gln Ser Ile
515 520 525

tct ggg gac cct gag ata gac aaa aaa atc aag aac cta aag aag aaa
1633
Ser Gly Asp Pro Glu Ile Asp Lys Lys Ile Lys Asn Leu Lys Lys Lys
530 535 540

ctg aaa gca atc gaa caa ctg aaa gaa caa gca gca act gga aaa cag
1681
Leu Lys Ala Ile Glu Gln Leu Lys Glu Gln Ala Ala Thr Gly Lys Gln
545 550 555

cta gaa aaa aat cag ttg gag aaa att cag aaa gaa aca gcc ctt ctc
1729

Leu Glu Lys Asn Gln Leu Glu Lys Ile Gln Lys Glu Thr Ala Leu Leu
560 565 570 575

cag gag ctg gaa gat ttg gaa ttg ggt att t aaagattcac ggaaagcaag
1780
Gln Glu Leu Glu Asp Leu Glu Leu Gly Ile
580 585

ttgatgacca gaaatcagtg caaacacatc ttctgttaaa cccattggta tacacagaat
1840
attcctgtgc ccacacttaa tgtcaatcta taattttaac catttatcca agattctact
1900
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1949

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Arg Glu Ser Gly Lys Asn Cys Lys Val Cys Ile Phe Ser Lys Asp Gly
35 40 45
Thr Leu Phe Ala Trp Gly Asn Gly Glu Lys Val Asn Ile Ile Ser Val
50 55 60
Thr Asn Lys Gly Leu Leu His Ser Phe Asp Leu Leu Lys Ala Val Cys
65 70 75 80
Leu Glu Phe Ser Pro Lys Asn Thr Val Leu Ala Thr Trp Gln Pro Tyr
85 90 95
Thr Thr Ser Lys Asp Gly Thr Ala Gly Ile Pro Asn Leu Gln Leu Tyr
100 105 110
Asp Val Lys Thr Gly Thr Cys Leu Lys Ser Phe Ile Gln Lys Lys Met
115 120 125
Gln Asn Trp Cys Pro Ser Trp Ser Glu Asp Glu Thr Leu Cys Ala Arg
130 135 140
Asn Val Asn Asn Glu Val His Phe Phe Glu Asn Asn Asn Phe Asn Thr
145 150 155 160
Ile Ala Asn Lys Leu His Leu Gln Lys Ile Asn Asp Phe Val Leu Ser
165 170 175
Pro Gly Pro Gln Pro Tyr Lys Val Ala Val Tyr Val Pro Gly Ser Lys
180 185 190
Gly Ala Pro Ser Phe Val Arg Leu Tyr Gln Tyr Pro Asn Phe Ala Gly
195 200 205
Pro His Ala Ala Leu Ala Asn Lys Ser Phe Phe Lys Ala Asp Lys Val
210 215 220
Thr Met Leu Trp Asn Lys Lys Ala Thr Ala Val Leu Val Ile Ala Ser
225 230 235 240
Thr Asp Val Asp Lys Thr Gly Ala Ser Tyr Tyr Gly Glu Gln Thr Leu
245 250 255
His Tyr Ile Ala Thr Asn Gly Glu Ser Ala Val Val Gln Leu Pro Lys
260 265 270
Asn Gly Pro Ile Tyr Asp Val Val Trp Asn Ser Ser Ser Thr Glu Phe
275 280 285

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Lys Cys Asp Pro Val Phe Asp Phe Gly Thr Gly Pro Arg Asn Ala Ala
305                 310                 315                 320
Tyr Tyr Ser Pro His Gly His Ile Leu Val Leu Ala Gly Phe Gly Asn
                325                 330                 335
Leu Arg Gly Gln Met Glu Val Trp Asp Val Lys Asn Tyr Lys Leu Ile
            340                 345                 350
Ser Lys Pro Val Ala Ser Asp Ser Thr Tyr Phe Ala Trp Cys Pro Asp
        355                 360                 365
Gly Glu His Ile Leu Thr Ala Thr Cys Ala Pro Arg Leu Arg Val Asn
    370                 375                 380
Asn Gly Tyr Lys Ile Trp His Tyr Thr Gly Ser Ile Leu His Lys Tyr
385                 390                 395                 400
Asp Val Pro Ser Asn Ala Glu Leu Trp Gln Val Ser Trp Gln Pro Phe
                405                 410                 415
Leu Asp Gly Ile Phe Pro Ala Lys Thr Ile Thr Tyr Gln Ala Val Pro
            420                 425                 430
Ser Glu Val Pro Asn Glu Glu Pro Lys Val Ala Thr Ala Tyr Arg Pro
        435                 440                 445
Pro Ala Leu Arg Asn Lys Pro Ile Thr Asn Ser Lys Leu His Glu Glu
    450                 455                 460
Glu Pro Pro Gln Asn Met Lys Pro Gln Ser Gly Asn Asp Lys Pro Leu
465                 470                 475                 480
Ser Lys Thr Ala Leu Lys Asn Gln Arg Lys His Glu Ala Lys Lys Ala
                485                 490                 495
Ala Lys Gln Glu Ala Arg Ser Asp Lys Ser Pro Asp Leu Ala Pro Thr
            500                 505                 510
Pro Ala Pro Gln Ser Thr Pro Arg Asn Thr Val Ser Gln Ser Ile Ser
        515                 520                 525
Gly Asp Pro Glu Ile Asp Lys Lys Ile Lys Asn Leu Lys Lys Lys Leu
    530                 535                 540
Lys Ala Ile Glu Gln Leu Lys Glu Gln Ala Ala Thr Gly Lys Gln Leu
545                 550                 555                 560
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110
Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly
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cca gat gag gag agt ttt ctg tac ttt gcc tac ggc agc aac ctg ctg
158

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aca gag agg atc cac ctc cga aac ccc tcg gcg gcg ttc ttc tgt gtg
206
Thr Glu Arg Ile His Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val
         30                  35                  40

gcc cgc ctg cag gat ttt aag ctt gac ttt ggc aat tcc caa ggc aaa
254
Ala Arg Leu Gln Asp Phe Lys Leu Asp Phe Gly Asn Ser Gln Gly Lys
     45                  50                  55

aca agt caa act tgg cat gga ggg ata gcc acc att ttt cag agt cct
302
Thr Ser Gln Thr Trp His Gly Gly Ile Ala Thr Ile Phe Gln Ser Pro
 60                  65                  70                  75

ggc gat gaa gtg tgg gga gta gta tgg aaa atg aac aaa agc aat tta
350
Gly Asp Glu Val Trp Gly Val Val Trp Lys Met Asn Lys Ser Asn Leu
                 80                  85                  90

aat tct ctg gat gag caa gaa ggg gtt aaa agt gga atg tat gtt gta
398
Asn Ser Leu Asp Glu Gln Glu Gly Val Lys Ser Gly Met Tyr Val Val
             95                  100                 105

ata gaa gtt aaa gtt gca act caa gaa gga aaa gaa ata acc tgt cga
446
Ile Glu Val Lys Val Ala Thr Gln Glu Gly Lys Glu Ile Thr Cys Arg
        110                 115                 120

agt tat ctg atg aca aat tac gaa agt gct ccc cca tcc cca cag tat
494
Ser Tyr Leu Met Thr Asn Tyr Glu Ser Ala Pro Pro Ser Pro Gln Tyr
    125                 130                 135

aaa aag att att tgc atg ggt gca aaa gaa aat ggt ttg ccg ctg gag
542
Lys Lys Ile Ile Cys Met Gly Ala Lys Glu Asn Gly Leu Pro Leu Glu
140                 145                 150                 155

tat caa gag aag tta aaa gca ata gaa cca aat gac tat aca gga aag
590
Tyr Gln Glu Lys Leu Lys Ala Ile Glu Pro Asn Asp Tyr Thr Gly Lys
                160                 165                 170

gtc tca gaa gaa att gaa gac atc atc aaa aag ggg gaa aca caa act
638
Val Ser Glu Glu Ile Glu Asp Ile Ile Lys Lys Gly Glu Thr Gln Thr
            175                 180                 185

ctt t agaacataac agaatatatc taagggtatt ctatgtgcta atataaaata
692
Leu
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ttttaacac ttgagaacag ggatctgggg gatctccacg tttgatccat tttcagcagt
752
gctctgaagg agtatcttac ttgggtgatt ccttgttttt agactataaa aagaaactgg
812
gataggagtt agacaattta aaaggggtgt atgagggcct gaaatatgtg acaaatgaat
872
gtgagtaccc cttctgtgaa cactgaaagc tattctcttg aattgatctt aagtgtctcc
932
ttgctctggt aaaagataga tttgtagctc acttgatgat ggtgctggtg aattgctctg
992
ctctgtctga gatttttaaa aatcagctta atgagagtaa tctgcagaca attgataata
1052
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1110

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Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val Ala Arg Leu Gln Asp
        35   40   45
Phe Lys Leu Asp Phe Gly Asn Ser Gln Gly Lys Thr Ser Gln Thr Trp
    50   55   60
His Gly Gly Ile Ala Thr Ile Phe Gln Ser Pro Gly Asp Glu Val Trp
65   70   75   80
Gly Val Val Trp Lys Met Asn Lys Ser Asn Leu Asn Ser Leu Asp Glu
                85   90   95
Gln Glu Gly Val Lys Ser Gly Met Tyr Val Val Ile Glu Val Lys Val
            100   105   110
Ala Thr Gln Glu Gly Lys Glu Ile Thr Cys Arg Ser Tyr Leu Met Thr
        115   120   125
Asn Tyr Glu Ser Ala Pro Pro Ser Pro Gln Tyr Lys Lys Ile Ile Cys
    130   135   140
Met Gly Ala Lys Glu Asn Gly Leu Pro Leu Glu Tyr Gln Glu Lys Leu
145   150   155   160
Lys Ala Ile Glu Pro Asn Asp Tyr Thr Gly Lys Val Ser Glu Glu Ile
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Glu Asp Ile Ile Lys Lys Gly Glu Thr Gln Thr Leu
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gcaggggcgt agtgggat atg gcc aac tcg ggc tgc aag gac gtc acg ggt
111
Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly
1 5 10

cca gat gag gag agt ttt ctg tac ttt gcc tac ggc agc aac ctg ctg
159
Pro Asp Glu Glu Ser Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu
15 20 25

aca gag agg atc cac ctc cga aac ccc tcg gcg gcg ttc ttc tgt gtg
207
Thr Glu Arg Ile His Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val
30 35 40

gcc cgc ctg cag gca aga agg ggt t aaaagtggaa tgtatgttgt
252
Ala Arg Leu Gln Ala Arg Arg Gly
45 50

aatagaagtt aaagttgcaa ctcaagaagg aaaagaaata acctgtcgaa gttatctgat
312
gacaaattac gaaagtgctc ccccatcccc acagtataaa aagattattt gcatgggtgc
372
aaaagaaaat ggtttgccgc tggagtatca agagaagtta aaagcaatag aaccaaatga
432
ctatacagga aaggtctcag aagaaattga agacatcatc aaaaaggggg aaacacaaac
492
tctttagaac ataacagaat atatctaagg gtattctatg tgctaatata aaatattttt
552
aacacttgag aacagggatc tgggggatct ccacgtttga tccattttca gcagtgctct
612
gaaggagtat cttacttggg tgattccttg tttttagact ataaaaagaa actgggatag
672
gagttagaca atttaaaagg ggtgtatgag ggcctgaaat atgtgacaaa tgaatgtgag
732
taccccttct gtgaacactg aaagctattc tcttgaattg atcttaagtg tctccttgct
792
ctggtaaaag atagatttgt agctcacttg atgatggtgc tggtgaattg ctctgctctg
852
tctgagattt ttaaaaatca gcttaatgag agtaatctgc agacaattga taataacatt
912
ttgaaaattg gaaagatggt atactgtttt tagaggaata aacgtatttg tgg
965

<210> 10
<211> 51
<212> PRT
<213> H. sapiens

<400> 10
Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly Pro Asp Glu Glu Ser
1 5 10 15
Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu Thr Glu Arg Ile His
20 25 30

Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val Ala Arg Leu Gln Ala
35 40 45
Arg Arg Gly
50

<210> 11
<211> 658
<212> DNA
<213> H. sapiens

<400> 11
tcgagaggag ctgacagcct tcctgcaccc cgaggagtga ggtgggccac tgggtgctgc
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cccctgccca ggaccagccc ctggtggaag ccaaccacct gctgcacgag agcgacacgg
120
acaaggacgg gcggctgagc aaagcggaaa tcctgggtaa ttggaacatg tttgtgggca
180
gtcaggccac caactatggt gaggacctga cccggcacca cgatgagctg tgagccccgc
240
gcacctgcca cagcctcaga ggcccgcaca atgaccggag gaggggccgc tgtggtctgg
300
ccccctccct gtccaggccc cgcaggaggc agatgcagtc ccaggcatcc tcctgccccc
360
gggctctcag ggaccccctg ggtcggcttc tgtccctgtc acacccccaa ccccagggag
420
gggctgtcat agtcccagag gataagcaat acctatttct gactgagtct cccagcccag
480
acccagggac cctggcccca agctcagctc taagaaccgc caccaacccc tccagctcca
540
aatctgagcc tccaccacat agactgaaac tcccctggcc ccagccctct cctgcctggc
600
ctggcctggg acacctcctc tctgccagga ggcaataaaa gccagcgccg ggaccttg
658

<210> 12
<211> 1507
<212> DNA
<213> H. sapiens

<220>
<221> misc_feature
<222> 1047, 1301
<223> n = A,T,C or G

<400> 12
ggaacgcaga gcggagcgtg gagagcggag cgaagctgga taacagggga ccgatgatgt
60
ggcgaccatc agttctgctg cttctgttgc tactgaggca cggggcccag gggaagccat
120
ccccagacgc aggccctcat ggccagggga gggtgcacca ggcggccccc ctgagcgacg
180
ctccccatga tgacgcccac gggaacttcc agtacgacca tgaggctttc ctgggacggg
240
aagtggccaa ggaattcgac caactcaccc cagaggaaag ccaggcccgt ctggggcgga
300
tcgtggaccg catggaccgc gcgggggacg gcgacggctg ggtgtcgctg gccgagcttc
360

gcgcgtggat cgcgcacacg cagcagcggc acatacggga ctcggtgagc gcggcctggg
420
acacgtacga cacggaccgc gacgggcgtg tgggttggga ggagctgcgc aacgccacct
480
atggccacta cgcgcccggt gaagaatttc atgacgtgga ggatgcagag acctacaaaa
540
agatgctggc tcgggacgag cggcgtttcc gggtggccga ccaggatggg gactcgatgg
600
ccactcgaga ggagctgaca gccttcctgc accccgagga gttccctcac atgcgggaca
660
tcgtgattgc tgaaaccctg gaggacctgg acagaaacaa agatggctat gtccaggtgg
720
aggagtacat cgcggatctg tactcagccg agcctgggga ggaggagccg gcgtgggtgc
780
agacggagag gcagcagttc cgggacttcc gggatctgaa caaggatggg cacctggatg
840
ggagtgaggt gggccactgg gtgctgcccc ctgcccagga ccagcccctg gtggaagcca
900
accacctgct gcacgaragc gacacggaca aggaygggcg gctgagcaaa gcgsaaatcc
960
tgggtaattg gaacatgttt gtgggcagtc aggccaccaa ctatggygag gacctgaccc
1020
ggcaccacga tgagctgtga gcmccgngca cctgccacag cctcagaggc ccgcacaatg
1080
accggaggag gggccgctgt ggtctggccc cctccctgtc caggccccgc aggaggcaga
1140
tgcagtccca ggcatcctcc tkcccctggg ctctcaggga ccccctgggt cggcttctgt
1200
ccctgtcaca cccccaaccc cagggagggg ctgtcatagt cccagaggat aagcaatacc
1260
tatttctgac tgagtctccc agcccagacc cagggaccct nggccccaag ctcagctcta
1320
agaaccgccc caacccctcc agctccaaat ctgagcctcc accacataga ctgaaactcc
1380
cctggcccca gccctctcct gcctggcctg gcctgggaca cctcctctct gccaggaggc
1440
aataaaagcc agcgccggga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1500
aaaaaan
1507

<210> 13
<211> 661
<212> DNA
<213> H. sapiens

<220>
<221> CDS
<222> (79)...(376)

<400> 13
ggcgcggtgc agggctctta agaacgaacg gcttgggcgc ggactggtat ccggggactg
60
tgacttgcag ggtccgcc atg gag cca gag cag atg ctg gag gga caa acg
111
Met Glu Pro Glu Gln Met Leu Glu Gly Gln Thr
1 5 10

cag gtt gca gaa aat cct cac tct gag tac ggt ctc aca gac aac gtt
159
Gln Val Ala Glu Asn Pro His Ser Glu Tyr Gly Leu Thr Asp Asn Val
15 20 25

gag aga ata gta gaa aat gag aag att aat gca gaa aag tca tca aag
207
Glu Arg Ile Val Glu Asn Glu Lys Ile Asn Ala Glu Lys Ser Ser Lys
30 35 40

cag aag gta gat ctc cag tct ttg cca act cgt gcc tac ctg gat cag
255
Gln Lys Val Asp Leu Gln Ser Leu Pro Thr Arg Ala Tyr Leu Asp Gln
45 50 55

aca gtt gtg cct atc tta tta cag gga ctt gct gtg ctt gca aag gaa
303
Thr Val Val Pro Ile Leu Leu Gln Gly Leu Ala Val Leu Ala Lys Glu
60 65 70 75

aga cca cca aat ccc att gaa ttt cta gca tct tat ctt tta aaa aac
351
Arg Pro Pro Asn Pro Ile Glu Phe Leu Ala Ser Tyr Leu Leu Lys Asn
80 85 90

aag gca cag ttt gaa gat cga aac t gacttaatgg gaagaacaga
396
Lys Ala Gln Phe Glu Asp Arg Asn
95

aaaatttagt tgctactgta gatttacatg attaagaggc agctttaatt gccatgatca
456
ttcctctttt ttggatgtat aagaaccttc cggacaacag aacctatttc tggaattgca
516
gaagataaca tatttccctt attttgattt aatcaccata aaccatacct atttaatgag
576
tgtattctgt gcaatttttt tctcagattg tctttaactt tgtttttaaa atgaccttca
636
aaataaactg tcaaaacacc attat
661

<210> 14
<211> 99
<212> PRT
<213> H. sapiens

<400> 14
Met Glu Pro Glu Gln Met Leu Glu Gly Gln Thr Gln Val Ala Glu Asn
1 5 10 15
Pro His Ser Glu Tyr Gly Leu Thr Asp Asn Val Glu Arg Ile Val Glu
20 25 30
Asn Glu Lys Ile Asn Ala Glu Lys Ser Ser Lys Gln Lys Val Asp Leu
35 40 45
Gln Ser Leu Pro Thr Arg Ala Tyr Leu Asp Gln Thr Val Val Pro Ile
50 55 60
Leu Leu Gln Gly Leu Ala Val Leu Ala Lys Glu Arg Pro Pro Asn Pro

65 70 75 80
Ile Glu Phe Leu Ala Ser Tyr Leu Leu Lys Asn Lys Ala Gln Phe Glu
85 90 95
Asp Arg Asn

<210> 15
<211> 1507
<212> DNA
<213> H. sapiens

<220>
<221> misc_feature
<222> 1047, 1301
<223> n = A,T,C or G

<400> 15
ggaacgcaga gcggagcgtg gagagcggag cgaagctgga taacagggga ccgatgatgt
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ggcgaccatc agttctgctg cttctgttgc tactgaggca cggggcccag gggaagccat
120
ccccagacgc aggccctcat ggccagggga gggtgcacca ggcggccccc ctgagcgacg
180
ctccccatga tgacgcccac gggaacttcc agtacgacca tgaggctttc ctgggacggg
240
aagtggccaa ggaattcgac caactcaccc cagaggaaag ccaggcccgt ctggggcgga
300
tcgtggaccg catggaccgc gcgggggacg gcgacggctg ggtgtcgctg gccgagcttc
360
gcgcgtggat cgcgcacacg cagcagcggc acatacggga ctcggtgagc gcggcctggg
420
acacgtacga cacggaccgc gacgggcgtg tgggttggga ggagctgcgc aacgccacct
480
atggccacta cgcgcccggt gaagaatttc atgacgtgga ggatgcagag acctacaaaa
540
agatgctggc tcgggacgag cggcgtttcc gggtggccga ccaggatggg gactcgatgg
600
ccactcgaga ggagctgaca gccttcctgc accccgagga gttccctcac atgcgggaca
660
tcgtgattgc tgaaaccctg gaggacctgg acagaaacaa agatggctat gtccaggtgg
720
aggagtacat cgcggatctg tactcagccg agcctgggga ggaggagccg gcgtgggtgc
780
agacggagag gcagcagttc cgggacttcc gggatctgaa caaggatggg cacctggatg
840
ggagtgaggt gggccactgg gtgctgcccc ctgcccagga ccagcccctg gtggaagcca
900
accacctgct gcacgaragc gacacggaca aggaygggcg gctgagcaaa gcgsaaatcc
960
tgggtaattg gaacatgttt gtgggcagtc aggccaccaa ctatggygag gacctgaccc
1020
ggcaccacga tgagctgtga gcmccgngca cctgccacag cctcagaggc ccgcacaatg
1080
accggaggag gggccgctgt ggtctggccc cctccctgtc caggccccgc aggaggcaga
1140
tgcagtccca ggcatcctcc tkcccctggg ctctcaggga ccccctgggt cggcttctgt
1200

ccctgtcaca cccccaaccc cagggagggg ctgtcatagt cccagaggat aagcaatacc
1260
tatttctgac tgagtctccc agcccagacc cagggaccct nggccccaag ctcagctcta
1320
agaaccgccc caacccctcc agctccaaat ctgagcctcc accacataga ctgaaactcc
1380
cctggcccca gccctctcct gcctggcctg gcctgggaca cctcctctct gccaggaggc
1440
aataaaagcc agcgccggga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1500
aaaaaan
1507

<210> 16
<211> 716
<212> DNA
<213> H. sapiens

<220>
<221> CDS
<222> (16)...(538)

<400> 16
ctcgatcgaa gcgag atg gcg gac gtg cta gat ctt cac gag gct ggg ggc
51
Met Ala Asp Val Leu Asp Leu His Glu Ala Gly Gly
1 5 10

gaa gat ttc gcc atg gat gag gat ggg gac gag agc att cac aaa ctg
99
Glu Asp Phe Ala Met Asp Glu Asp Gly Asp Glu Ser Ile His Lys Leu
15 20 25

aaa gaa aaa gcg aag aaa cgg aag ggt cgc ggc ttt ggc tcc gaa gag
147
Lys Glu Lys Ala Lys Lys Arg Lys Gly Arg Gly Phe Gly Ser Glu Glu
30 35 40

ggg tcc cga gcg cgg atg cgt gag gat tat gac agc gtg gag cag gat
195
Gly Ser Arg Ala Arg Met Arg Glu Asp Tyr Asp Ser Val Glu Gln Asp
45 50 55 60

ggc gat gaa ccc gga cca caa cgc tct gtt gaa ggc tgg att ctc ttt
243
Gly Asp Glu Pro Gly Pro Gln Arg Ser Val Glu Gly Trp Ile Leu Phe
65 70 75

gta act gga gtc cat gag gaa gcc acc gaa gaa gac ata cac gac aaa
291
Val Thr Gly Val His Glu Glu Ala Thr Glu Glu Asp Ile His Asp Lys
80 85 90

ttc gca gaa tat ggg gaa att aaa aac att cat ctc aac ctc gac agg
339
Phe Ala Glu Tyr Gly Glu Ile Lys Asn Ile His Leu Asn Leu Asp Arg
95 100 105

cga aca gga tat ctg aag ggg tat act cta gtt gaa tat gaa aca tac
387
Arg Thr Gly Tyr Leu Lys Gly Tyr Thr Leu Val Glu Tyr Glu Thr Tyr
110 115 120

aag gaa gcc cag gct gct atg gag gga ctc aat ggc cag gat ttg atg
435
Lys Glu Ala Gln Ala Ala Met Glu Gly Leu Asn Gly Gln Asp Leu Met
125 130 135 140

gga cag ccc atc agc gtt gac tgg tgt ttt gtt cgg ggt cca cca aaa
483
Gly Gln Pro Ile Ser Val Asp Trp Cys Phe Val Arg Gly Pro Pro Lys
145 150 155

ggc aag agg aga ggt ggc cga aga cgc agc aga agt cca gac cgg aga
531
Gly Lys Arg Arg Gly Gly Arg Arg Arg Ser Arg Ser Pro Asp Arg Arg
160 165 170

cgt cgc t gacaggtcct ctgttgtcca ggtgttctct tcaagattcc atttgaccat
588
Arg Arg

gcagccttgg acaaatagga ctggggtgga acttgctgtg tttatattta atctcttacc
648
gtatatgcgt agtatttgag ttgcgaataa atgttccatt ttgttttcta caaaaaaaaa
708
aaaaaaaa
716

<210> 17
<211> 174
<212> PRT
<213> H. sapiens

<400> 17
Met Ala Asp Val Leu Asp Leu His Glu Ala Gly Gly Glu Asp Phe Ala
1 5 10 15
Met Asp Glu Asp Gly Asp Glu Ser Ile His Lys Leu Lys Glu Lys Ala
20 25 30
Lys Lys Arg Lys Gly Arg Gly Phe Gly Ser Glu Glu Gly Ser Arg Ala
35 40 45
Arg Met Arg Glu Asp Tyr Asp Ser Val Glu Gln Asp Gly Asp Glu Pro
50 55 60
Gly Pro Gln Arg Ser Val Glu Gly Trp Ile Leu Phe Val Thr Gly Val
65 70 75 80
His Glu Glu Ala Thr Glu Glu Asp Ile His Asp Lys Phe Ala Glu Tyr
85 90 95
Gly Glu Ile Lys Asn Ile His Leu Asn Leu Asp Arg Arg Thr Gly Tyr
100 105 110
Leu Lys Gly Tyr Thr Leu Val Glu Tyr Glu Thr Tyr Lys Glu Ala Gln
115 120 125
Ala Ala Met Glu Gly Leu Asn Gly Gln Asp Leu Met Gly Gln Pro Ile
130 135 140

Ser Val Asp Trp Cys Phe Val Arg Gly Pro Pro Lys Gly Lys Arg Arg
145 150 155 160
Gly Gly Arg Arg Arg Ser Arg Ser Pro Asp Arg Arg Arg Arg
165 170

<210> 18
<211> 763
<212> DNA
<213> H. sapiens

<220>
<221> CDS
<222> (2)...(551)

<400> 18
c atg gcc aag ccg tgt ggg gtg cgc ctg agc ggg gaa gcc cgc aaa cag
49
Met Ala Lys Pro Cys Gly Val Arg Leu Ser Gly Glu Ala Arg Lys Gln
1 5 10 15

gtg gag gtc ttc aga cag aat ctt ttc cag gag gct gag gaa ttc ctc
97
Val Glu Val Phe Arg Gln Asn Leu Phe Gln Glu Ala Glu Glu Phe Leu
20 25 30

tac aga ttc ttg cca cag aaa atc ata tac ctg aat cag ctc ttg caa
145
Tyr Arg Phe Leu Pro Gln Lys Ile Ile Tyr Leu Asn Gln Leu Leu Gln
35 40 45

gag gac tcc ctc aat gtg gct gac ttg act tcc ctc cgg gcc cca ctg
193
Glu Asp Ser Leu Asn Val Ala Asp Leu Thr Ser Leu Arg Ala Pro Leu
50 55 60

gac atc ccc atc cca gac cct cca ccc aag gat gat gag atg gaa aca
241
Asp Ile Pro Ile Pro Asp Pro Pro Pro Lys Asp Asp Glu Met Glu Thr
65 70 75 80

gat aag cag gag aag aaa gaa gtc cct aag tgt gga ttt ctc cct ggg
289
Asp Lys Gln Glu Lys Lys Glu Val Pro Lys Cys Gly Phe Leu Pro Gly
85 90 95

aat gag aaa gtc ctg tcc ctg ctt gcc ctg gtt aag cca gaa gtc tgg
337
Asn Glu Lys Val Leu Ser Leu Leu Ala Leu Val Lys Pro Glu Val Trp
100 105 110

act ctc aaa gag aaa tgc att ctg gtg att aca tgg atc caa cac ctg
385
Thr Leu Lys Glu Lys Cys Ile Leu Val Ile Thr Trp Ile Gln His Leu
115 120 125

atc ccc aag att gaa gat gga aat gat ttt ggg gta gca atc cag gag
433
Ile Pro Lys Ile Glu Asp Gly Asn Asp Phe Gly Val Ala Ile Gln Glu

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    130                 135                 140

aag gtg ctg gag agg gtg aat gcc gtc aag acc aaa gtg aag ctt tcc
481
Lys Val Leu Glu Arg Val Asn Ala Val Lys Thr Lys Val Lys Leu Ser
145                 150                 155                 160

aga caa cca ttt cca agt act tct cag aac gtg ggg atg ctg tgg cca
529
Arg Gln Pro Phe Pro Ser Thr Ser Gln Asn Val Gly Met Leu Trp Pro
                165                 170                 175

agg cct cca agg aga ctc atg t aatggattac cgggccttgg tgcatgagcg
581
Arg Pro Pro Arg Arg Leu Met
            180

agatgaggca gcctatgggg agctcagggc catggtgctg gacctgaggg ccttctatgc
641
tgagctttat catatcatca gcagcaacct ggagaaaatt gtcaacccaa agggtgaaga
701
aaagccatct atgtactgaa cccgggacta gaaggaaaat aaatgatcta tatgttgtgt
761
gg
763

<210> 19
<211> 183
<212> PRT
<213> H. sapiens

<400> 19
Met Ala Lys Pro Cys Gly Val Arg Leu Ser Gly Glu Ala Arg Lys Gln
 1               5                  10                  15
Val Glu Val Phe Arg Gln Asn Leu Phe Gln Glu Ala Glu Glu Phe Leu
            20                  25                  30
Tyr Arg Phe Leu Pro Gln Lys Ile Ile Tyr Leu Asn Gln Leu Leu Gln
        35                  40                  45
Glu Asp Ser Leu Asn Val Ala Asp Leu Thr Ser Leu Arg Ala Pro Leu
    50                  55                  60
Asp Ile Pro Ile Pro Asp Pro Pro Pro Lys Asp Asp Glu Met Glu Thr
65                  70                  75                  80
Asp Lys Gln Glu Lys Lys Glu Val Pro Lys Cys Gly Phe Leu Pro Gly
                85                  90                  95
Asn Glu Lys Val Leu Ser Leu Leu Ala Leu Val Lys Pro Glu Val Trp
            100                 105                 110
Thr Leu Lys Glu Lys Cys Ile Leu Val Ile Thr Trp Ile Gln His Leu
        115                 120                 125
Ile Pro Lys Ile Glu Asp Gly Asn Asp Phe Gly Val Ala Ile Gln Glu
    130                 135                 140
Lys Val Leu Glu Arg Val Asn Ala Val Lys Thr Lys Val Lys Leu Ser
145                 150                 155                 160
Arg Gln Pro Phe Pro Ser Thr Ser Gln Asn Val Gly Met Leu Trp Pro
                165                 170                 175
Arg Pro Pro Arg Arg Leu Met
            180
<210> 20
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<211> 790
<212> DNA
<213> H. sapiens

<220>
<221> CDS
<222> (240)...(585)

<400> 20
acgttttaca gtctttaatt aagcacataa aactgtacta tttaatatat ttctccatga
60
actttttgtg aaattcagat cgcagtgtgt catttacaaa tcttttgtct ttcttctggt
120
catctacacc ttttgcacag ttcttgaaga caacgtcatc atcccacctt cttttaactt
180
tgaagttggc ctgaggctgg gatgggccag tgagattaag gagagggttt ccgctcaga
239
atg ttt tcc ata cga atc ctc tct tct tca gct ttt tgt tct tgt tcc
287
Met Phe Ser Ile Arg Ile Leu Ser Ser Ser Ala Phe Cys Ser Cys Ser
 1   5   10   15

ttc ctg gcc tgc tct tca gct ctt tct ttt tta att ttt tcc agt tct
335
Phe Leu Ala Cys Ser Ser Ala Leu Ser Phe Leu Ile Phe Ser Ser Ser
             20   25   30

gca aga aga gct gca gta tca tca tca tca ctt tct tct tca aaa tct
383
Ala Arg Arg Ala Ala Val Ser Ser Ser Ser Leu Ser Ser Ser Lys Ser
         35   40   45

tca tct tcc tca tct gtt aga ggg tca tct gca tca agg ttg gcg gca
431
Ser Ser Ser Ser Ser Val Arg Gly Ser Ser Ala Ser Arg Leu Ala Ala
     50   55   60

gga atc tgg tct aac cgt ggc ttt ttt gac act gaa gag gag gtt gta
479
Gly Ile Trp Ser Asn Arg Gly Phe Phe Asp Thr Glu Glu Glu Val Val
 65   70   75   80

tgt tct cgg gtt gga cga tcc cta ttt ttc tct ctt gca gca gct ctc
527
Cys Ser Arg Val Gly Arg Ser Leu Phe Phe Ser Leu Ala Ala Ala Leu
                 85   90   95

tct ctt tct tcc aac tct ctc ctg aag tca cgg tta cga acc tct tca
575
Ser Leu Ser Ser Asn Ser Leu Leu Lys Ser Arg Leu Arg Thr Ser Ser
            100   105   110

ggg gca tcc t gagtagtctg tctgtatttt atctttgtat gagagggtag
625
Gly Ala Ser
        115

gtctctgctt gaatactgct ttgaaagttg gctcaaatca ccttctcctt ttccccttcc
685
acctctggca ggttcaaagg ttggcctggc tgctgttgtc atcttttatg actggccgag
745
gtccgatgca gcaggctccg aagatcatac agacgccatt accac
790

<210> 21
<211> 115
<212> PRT
<213> H. sapiens

<400> 21
Met Phe Ser Ile Arg Ile Leu Ser Ser Ser Ala Phe Cys Ser Cys Ser
 1   5   10   15
Phe Leu Ala Cys Ser Ser Ala Leu Ser Phe Leu Ile Phe Ser Ser Ser
            20   25   30
Ala Arg Arg Ala Ala Val Ser Ser Ser Ser Leu Ser Ser Ser Lys Ser
        35   40   45
Ser Ser Ser Ser Ser Val Arg Gly Ser Ser Ala Ser Arg Leu Ala Ala
    50   55   60
Gly Ile Trp Ser Asn Arg Gly Phe Phe Asp Thr Glu Glu Glu Val Val
65   70   75   80
Cys Ser Arg Val Gly Arg Ser Leu Phe Phe Ser Leu Ala Ala Ala Leu
                85   90   95
Ser Leu Ser Ser Asn Ser Leu Leu Lys Ser Arg Leu Arg Thr Ser Ser
            100   105   110
Gly Ala Ser
        115
<210> 22
<211> 1939
<212> DNA
<213> H. sapiens

<220>
<221> CDS
<222> (53)...(1700)

<400> 22
gtggcgccag cggaggcagg ttgctgtgtt tgtgcttcct tctacagcca at atg aaa
58
                                                          Met Lys
                                                           1

agg cct aag tta aag aaa gca agt aaa cgc atg acc tgc cat aag cgg
106
Arg Pro Lys Leu Lys Lys Ala Ser Lys Arg Met Thr Cys His Lys Arg
         5   10   15

tat aaa atc caa aaa aag gtt cga gaa cat cat cga aaa tta aga aag
154
Tyr Lys Ile Gln Lys Lys Val Arg Glu His His Arg Lys Leu Arg Lys
     20   25   30

gag gct aaa aag cag ggt cac aag aag cct agg aaa gac cca gga gtt
202
Glu Ala Lys Lys Gln Gly His Lys Lys Pro Arg Lys Asp Pro Gly Val

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 35                  40                  45                  50

cca aac agt gct ccc ttt aag gag gct ctt ctt agg gaa gct gag cta
250
Pro Asn Ser Ala Pro Phe Lys Glu Ala Leu Leu Arg Glu Ala Glu Leu
                 55                  60                  65

agg aaa cag agg ctt gaa gaa cta aaa cag cag cag aaa ctt gac agg
298
Arg Lys Gln Arg Leu Glu Glu Leu Lys Gln Gln Gln Lys Leu Asp Arg
             70                  75                  80

cag aag gaa cta gaa aag aaa aga aaa ctt gaa act aat cct gat att
346
Gln Lys Glu Leu Glu Lys Lys Arg Lys Leu Glu Thr Asn Pro Asp Ile
         85                  90                  95

aag cca tca aat gtg gaa cct atg gaa aag gag ttt ggg ctt tgc aaa
394
Lys Pro Ser Asn Val Glu Pro Met Glu Lys Glu Phe Gly Leu Cys Lys
    100                 105                 110

act gag aac aaa gcc aag tcg ggc aaa cag aat tca aag aag ctg tac
442
Thr Glu Asn Lys Ala Lys Ser Gly Lys Gln Asn Ser Lys Lys Leu Tyr
115                 120                 125                 130

tgc caa gaa ctt aaa aag gtg att gaa gcc tcc gat gtt gtc cta gag
490
Cys Gln Glu Leu Lys Lys Val Ile Glu Ala Ser Asp Val Val Leu Glu
                135                 140                 145

gtg ttg gat gcc aga gat cct ctt ggt tgc aga tgt cct cag gta gaa
538
Val Leu Asp Ala Arg Asp Pro Leu Gly Cys Arg Cys Pro Gln Val Glu
            150                 155                 160

gag gcc att gtc cag agt gga cag aaa aag ctg gta ctt ata tta aat
586
Glu Ala Ile Val Gln Ser Gly Gln Lys Lys Leu Val Leu Ile Leu Asn
        165                 170                 175

aaa tca gat ctg gta cca aag gag aat ttg gag agc tgg cta aat tat
634
Lys Ser Asp Leu Val Pro Lys Glu Asn Leu Glu Ser Trp Leu Asn Tyr
    180                 185                 190

ttg aag aaa gaa ttg cca aca gtg gtg ttc aga gcc tca aca aaa cca
682
Leu Lys Lys Glu Leu Pro Thr Val Val Phe Arg Ala Ser Thr Lys Pro
195                 200                 205                 210

aag gat aaa ggg aag ata acc aag cgt gtg aag gca aag aag aat gct
730
Lys Asp Lys Gly Lys Ile Thr Lys Arg Val Lys Ala Lys Lys Asn Ala
                215                 220                 225
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gct cca ttc aga agt gaa gtc tgc ttt ggg aaa gag ggc ctt tgg aaa
778
Ala Pro Phe Arg Ser Glu Val Cys Phe Gly Lys Glu Gly Leu Trp Lys
            230                 235                 240

ctt ctt gga ggt ttt cag gaa act tgc agc aaa gcc att cgg gtt gga
826
Leu Leu Gly Gly Phe Gln Glu Thr Cys Ser Lys Ala Ile Arg Val Gly
        245                 250                 255

gta att ggt ttc cca aat gtg ggg aaa agc agc att atc aat agc tta
874
Val Ile Gly Phe Pro Asn Val Gly Lys Ser Ser Ile Ile Asn Ser Leu
    260                 265                 270

aaa caa gaa cag atg tgt aat gtt ggt gta tcc atg ggg ctt aca agg
922
Lys Gln Glu Gln Met Cys Asn Val Gly Val Ser Met Gly Leu Thr Arg
275                 280                 285                 290

agc atg caa gtt gtc ccc ttg gac aaa cag atc aca atc ata gat agt
970
Ser Met Gln Val Val Pro Leu Asp Lys Gln Ile Thr Ile Ile Asp Ser
                295                 300                 305

ccg agc ttc atc gta tct cca ctt aat tcc tcc tct gcg ctt gct ctg
1018
Pro Ser Phe Ile Val Ser Pro Leu Asn Ser Ser Ser Ala Leu Ala Leu
            310                 315                 320

cga agt cca gca agt att gaa gta gta aaa ccg atg gag gct gcc agt
1066
Arg Ser Pro Ala Ser Ile Glu Val Val Lys Pro Met Glu Ala Ala Ser
        325                 330                 335

gcc atc ctt tcc cag gct gat gct cga cag gta gta ctg aaa tat act
1114
Ala Ile Leu Ser Gln Ala Asp Ala Arg Gln Val Val Leu Lys Tyr Thr
    340                 345                 350

gtc cca ggc tac agg aat tct ctg gaa ttt ttt act atg ctt gct cag
1162
Val Pro Gly Tyr Arg Asn Ser Leu Glu Phe Phe Thr Met Leu Ala Gln
355                 360                 365                 370

aga aga ggt atg cac caa aaa ggt gga atc cca aat gtt gaa ggt gct
1210
Arg Arg Gly Met His Gln Lys Gly Gly Ile Pro Asn Val Glu Gly Ala
                375                 380                 385

gcc aaa ctg ctg tgg tct gag tgg aca ggt gcc tca tta gct tac tat
1258
Ala Lys Leu Leu Trp Ser Glu Trp Thr Gly Ala Ser Leu Ala Tyr Tyr
            390                 395                 400

tgc cat ccc cct aca tct tgg act cct cct cca tat ttt aat gag agt
1306
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Cys His Pro Pro Thr Ser Trp Thr Pro Pro Pro Tyr Phe Asn Glu Ser
        405                 410                 415

att gtg gta gac atg aaa agc ggc ttc aat ctg gaa gaa ctg gaa aag
1354
Ile Val Val Asp Met Lys Ser Gly Phe Asn Leu Glu Glu Leu Glu Lys
    420                 425                 430

aac aat gca cag agc ata aga gcc atc aag ggc cct cat ttg gcc aat
1402
Asn Asn Ala Gln Ser Ile Arg Ala Ile Lys Gly Pro His Leu Ala Asn
435                 440                 445                 450

agc atc ctt ttc cag tct tcc ggt ctg aca aat gga ata ata gaa gaa
1450
Ser Ile Leu Phe Gln Ser Ser Gly Leu Thr Asn Gly Ile Ile Glu Glu
                455                 460                 465

aag gac ata cat gaa gaa ttg cca aaa cgg aaa gaa agg aag cag gag
1498
Lys Asp Ile His Glu Glu Leu Pro Lys Arg Lys Glu Arg Lys Gln Glu
            470                 475                 480

gag agg gag gat gac aaa gac agt gac cag gaa act gtt gat gaa gaa
1546
Glu Arg Glu Asp Asp Lys Asp Ser Asp Gln Glu Thr Val Asp Glu Glu
        485                 490                 495

gtt gat gaa aac agc tca ggc atg ttt gct gca gaa gag aca ggg gag
1594
Val Asp Glu Asn Ser Ser Gly Met Phe Ala Ala Glu Glu Thr Gly Glu
    500                 505                 510

gca ctg tct gag gag act aca gca ggt gaa cag tct aca agg tct ttt
1642
Ala Leu Ser Glu Glu Thr Thr Ala Gly Glu Gln Ser Thr Arg Ser Phe
515                 520                 525                 530

atc ttg gat aaa atc att gaa gag gat gat gct tat gac ttc agt aca
1690
Ile Leu Asp Lys Ile Ile Glu Glu Asp Asp Ala Tyr Asp Phe Ser Thr
                535                 540                 545

gat tat gtg t aacagaacaa tggcttttta tgatttttt ttttaacatt
1740
Asp Tyr Val


ttaagcagac tgctaaactg ttctctgtat aagttatggt atgcatgagc tgtgtaaatt
1800
ttgtgaatat gtattatatt aaaaccaggc aacttggaat ccctaaattc tgtaaaaaga
1860
caattcatct cattgtgagt ggaagtagtt atctggaata aaaaaagaag atacctattg
1920
aaaaaaaaaa aaaaaaaaa
1939
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<210> 23
<211> 549
<212> PRT
<213> H. sapiens

<400> 23
Met Lys Arg Pro Lys Leu Lys Lys Ala Ser Lys Arg Met Thr Cys His
 1   5   10   15
Lys Arg Tyr Lys Ile Gln Lys Lys Val Arg Glu His His Arg Lys Leu
            20   25   30
Arg Lys Glu Ala Lys Lys Gln Gly His Lys Lys Pro Arg Lys Asp Pro
        35   40   45
Gly Val Pro Asn Ser Ala Pro Phe Lys Glu Ala Leu Leu Arg Glu Ala
    50   55   60
Glu Leu Arg Lys Gln Arg Leu Glu Glu Leu Lys Gln Gln Gln Lys Leu
65   70   75   80
Asp Arg Gln Lys Glu Leu Glu Lys Lys Arg Lys Leu Glu Thr Asn Pro
                85   90   95
Asp Ile Lys Pro Ser Asn Val Glu Pro Met Glu Lys Glu Phe Gly Leu
            100   105   110
Cys Lys Thr Glu Asn Lys Ala Lys Ser Gly Lys Gln Asn Ser Lys Lys
        115   120   125
Leu Tyr Cys Gln Glu Leu Lys Lys Val Ile Glu Ala Ser Asp Val Val
    130   135   140
Leu Glu Val Leu Asp Ala Arg Asp Pro Leu Gly Cys Arg Cys Pro Gln
145   150   155   160
Val Glu Glu Ala Ile Val Gln Ser Gly Gln Lys Lys Leu Val Leu Ile
                165   170   175
Leu Asn Lys Ser Asp Leu Val Pro Lys Glu Asn Leu Glu Ser Trp Leu
            180   185   190
Asn Tyr Leu Lys Lys Glu Leu Pro Thr Val Val Phe Arg Ala Ser Thr
        195   200   205
Lys Pro Lys Asp Lys Gly Lys Ile Thr Lys Arg Val Lys Ala Lys Lys
    210   215   220
Asn Ala Ala Pro Phe Arg Ser Glu Val Cys Phe Gly Lys Glu Gly Leu
225   230   235   240
Trp Lys Leu Leu Gly Gly Phe Gln Glu Thr Cys Ser Lys Ala Ile Arg
                245   250   255
Val Gly Val Ile Gly Phe Pro Asn Val Gly Lys Ser Ser Ile Ile Asn
            260   265   270
Ser Leu Lys Gln Glu Gln Met Cys Asn Val Gly Val Ser Met Gly Leu
        275   280   285
Thr Arg Ser Met Gln Val Val Pro Leu Asp Lys Gln Ile Thr Ile Ile
    290   295   300
Asp Ser Pro Ser Phe Ile Val Ser Pro Leu Asn Ser Ser Ser Ala Leu
305   310   315   320
Ala Leu Arg Ser Pro Ala Ser Ile Glu Val Val Lys Pro Met Glu Ala
                325   330   335
Ala Ser Ala Ile Leu Ser Gln Ala Asp Ala Arg Gln Val Val Leu Lys
            340   345   350
Tyr Thr Val Pro Gly Tyr Arg Asn Ser Leu Glu Phe Phe Thr Met Leu
        355   360   365
Ala Gln Arg Arg Gly Met His Gln Lys Gly Gly Ile Pro Asn Val Glu
    370   375   380
Gly Ala Ala Lys Leu Leu Trp Ser Glu Trp Thr Gly Ala Ser Leu Ala
385   390   395   400
Tyr Tyr Cys His Pro Pro Thr Ser Trp Thr Pro Pro Pro Tyr Phe Asn

```
                405                 410                 415
Glu Ser Ile Val Val Asp Met Lys Ser Gly Phe Asn Leu Glu Glu Leu
            420                 425                 430
Glu Lys Asn Asn Ala Gln Ser Ile Arg Ala Ile Lys Gly Pro His Leu
        435                 440                 445
Ala Asn Ser Ile Leu Phe Gln Ser Ser Gly Leu Thr Asn Gly Ile Ile
    450                 455                 460
Glu Glu Lys Asp Ile His Glu Glu Leu Pro Lys Arg Lys Glu Arg Lys
465                 470                 475                 480
Gln Glu Glu Arg Glu Asp Asp Lys Asp Ser Asp Gln Glu Thr Val Asp
                485                 490                 495
Glu Glu Val Asp Glu Asn Ser Ser Gly Met Phe Ala Ala Glu Glu Thr
            500                 505                 510
Gly Glu Ala Leu Ser Glu Glu Thr Thr Ala Gly Glu Gln Ser Thr Arg
        515                 520                 525
Ser Phe Ile Leu Asp Lys Ile Ile Glu Glu Asp Asp Ala Tyr Asp Phe
    530                 535                 540
Ser Thr Asp Tyr Val
545
<210> 24
<211> 503
<212> DNA
<213> H. sapiens

<220>
<221> CDS
<222> (10)...(400)

<400> 24
ggccacgta atg tcc gta gtt cgc tca tcc gtc cat gcc aga tgg att gtg
51
          Met Ser Val Val Arg Ser Ser Val His Ala Arg Trp Ile Val
           1               5                  10

ggg aag gtg att ggg aca aaa atg caa aag act gct aaa gtg aga gtg
99
Gly Lys Val Ile Gly Thr Lys Met Gln Lys Thr Ala Lys Val Arg Val
 15                  20                  25                  30

acc agg ctt gtt ctg gat ccc tat tta tta aag tat ttt aat aag cgg
147
Thr Arg Leu Val Leu Asp Pro Tyr Leu Leu Lys Tyr Phe Asn Lys Arg
                 35                  40                  45

aaa acc tac ttt gct cac gat gcc ctt cag cag tgc aca gtt ggg gat
195
Lys Thr Tyr Phe Ala His Asp Ala Leu Gln Gln Cys Thr Val Gly Asp
            50                  55                  60

att gtg ctt ctc aga gct tta cct gtt cca cga gca aag cat gtg aaa
243
Ile Val Leu Leu Arg Ala Leu Pro Val Pro Arg Ala Lys His Val Lys
        65                  70                  75

cat gaa ctg gct gag atc gtt ttc aaa gtt gga aaa gtc ata gat cca
291
His Glu Leu Ala Glu Ile Val Phe Lys Val Gly Lys Val Ile Asp Pro
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     80                  85                  90

gtg aca gga aag ccc tgt gct gga act acc tac ctg gag agt ccg ttg
339
Val Thr Gly Lys Pro Cys Ala Gly Thr Thr Tyr Leu Glu Ser Pro Leu
 95                 100                 105                 110

agt tcg gaa acc acc cag cta agc aaa aat ctg gaa gaa ctc aat atc
387
Ser Ser Glu Thr Thr Gln Leu Ser Lys Asn Leu Glu Glu Leu Asn Ile
                115                 120                 125

tct tca gca cag t gaagcgggag tggaagaagg atctgaaggg aaaaactgac
440
Ser Ser Ala Gln
            130

atgtttatgt tatggaaaaa gaaatttttc taagtttcat cacaaaaaaa aaaaaaaaaa
500
aaa
503

<210> 25
<211> 130
<212> PRT
<213> H. sapiens

<400> 25
Met Ser Val Val Arg Ser Ser Val His Ala Arg Trp Ile Val Gly Lys
 1               5                  10                  15
Val Ile Gly Thr Lys Met Gln Lys Thr Ala Lys Val Arg Val Thr Arg
            20                  25                  30
Leu Val Leu Asp Pro Tyr Leu Leu Lys Tyr Phe Asn Lys Arg Lys Thr
        35                  40                  45
Tyr Phe Ala His Asp Ala Leu Gln Gln Cys Thr Val Gly Asp Ile Val
    50                  55                  60
Leu Leu Arg Ala Leu Pro Val Pro Arg Ala Lys His Val Lys His Glu
65                  70                  75                  80
Leu Ala Glu Ile Val Phe Lys Val Gly Lys Val Ile Asp Pro Val Thr
                85                  90                  95
Gly Lys Pro Cys Ala Gly Thr Thr Tyr Leu Glu Ser Pro Leu Ser Ser
            100                 105                 110
Glu Thr Thr Gln Leu Ser Lys Asn Leu Glu Glu Leu Asn Ile Ser Ser
        115                 120                 125
Ala Gln
    130
<210> 26
<211> 651
<212> DNA
<213> H. sapiens

<400> 26
ggaattcggc acgaggtcga ctcctgtgag gtatggtgct gggtgcagat gcagtgtggc
60
tctggatagc accttatgga cagttgtgtc cccaaggaag gatgagaata gctactgaag
120
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tcctaaagag caagcctaac tcaagccatt ggcacacagg cattagacag aaagctggaa
180
gttgaaatgg tggagtccaa cttgcctgga ccagcttaat ggttctgctc ctggtaacgt
240
ttttatccat ggatgacttg cttgggtaag gacatgaaga cagttcctgt catacctttt
300
aaaggtatgg agagtcggct tgactacact gtgtggagca agttttaaag aagcaaagga
360
ctcagaattc atgattgaag aaatgcaggc agacctgtta tcctaaacta gggtttttaa
420
tgaccacaac aagcaagcat gcagcttact gcttgaaagg gtcttgcctc acccaagcta
480
gagtgcagtg gcctttgaag cttactacag cctcaaactt ctgggctcaa gtgatcctca
540
gcctcccagt ggtctttgta gactgcctga tggagtctca tggcacaaga agattaaaac
600
agtgtctcca attttaataa atttttgcaa tccaaaaaaa aaaaaaaaaa a
651

<210> 27
<211> 559
<212> DNA
<213> H. sapiens

<220>
<221> CDS
<222> (324)...(519)

<400> 27
ggctctggat agcaccttat ggacagttgt gtccccaagg aaggatgaga atagctactg
60
aagtcctaaa gagcaagcct aactcaagcc attggcacac aggcattaga cagaaagctg
120
gaagttgaaa tggtggagtc caacttgcct ggaccagctt aatggttctg ctcctggtaa
180
cgtttttatc catggatgac ttgcttgggt atggagagtc ggcttgacta cactgtgtgg
240
agcaagtttt aaagaagcaa aggactcaga attcatgatt gaagaaatgc aggcagacct
300
gttatcctaa actagggttt tta atg acc aca aca agc aag cat gca gct tac
353
Met Thr Thr Thr Ser Lys His Ala Ala Tyr
1 5 10

tgc ttg aaa ggg tct tgc ctc acc caa gct aga gtg cag tgg cct ttg
401
Cys Leu Lys Gly Ser Cys Leu Thr Gln Ala Arg Val Gln Trp Pro Leu
15 20 25

aag ctt act aca gcc tca aac ttc tgg gct caa gtg atc ctc agc ctc
449
Lys Leu Thr Thr Ala Ser Asn Phe Trp Ala Gln Val Ile Leu Ser Leu
30 35 40

cca gtg gtc ttt gta gac tgc ctg atg gag tct cat ggc aca aga aga
497
Pro Val Val Phe Val Asp Cys Leu Met Glu Ser His Gly Thr Arg Arg

45 50 55

tta aaa cag tgt ctc caa ttt t aataaatttt tgcaatccaa aaaaaaaaaa
549
Leu Lys Gln Cys Leu Gln Phe
60 65

aaaaaaaaaa
559

<210> 28
<211> 65
<212> PRT
<213> H. sapiens

<400> 28
Met Thr Thr Thr Ser Lys His Ala Ala Tyr Cys Leu Lys Gly Ser Cys
1 5 10 15
Leu Thr Gln Ala Arg Val Gln Trp Pro Leu Lys Leu Thr Thr Ala Ser
20 25 30
Asn Phe Trp Ala Gln Val Ile Leu Ser Leu Pro Val Val Phe Val Asp
35 40 45
Cys Leu Met Glu Ser His Gly Thr Arg Arg Leu Lys Gln Cys Leu Gln
50 55 60
Phe
65
<210> 29
<211> 623
<212> DNA
<213> H. sapiens

<220>
<223> primer sequence

<400> 29
tcgagcggcc gcccgggcag gtgtcgactc ctgtgaggta tggtgctggg tgcagatgca
60
gtgtggctct ggatagcacc ttatggacag ttgtgtcccc aaggaaggat gagaatagct
120
actgaagtcc taaagagcaa gcctaactca agccattggc acacaggcat tagacagaaa
180
gctggaagtt gaaatggtgg agtccaactt gcctggacca gcttaatggt tctgctcctg
240
gtaacgtttt tatccatgga tgacttgctt gggtatggag agtcggcttg actacactgt
300
gtggagcaag ttttaaagaa gcaaaggact cagaattcat gattgaagaa atgcaggcag
360
acctgttatc ctaaactagg gtttttaatg accacaacaa gcaagcatgc agcttactgc
420
ttgaaagggt cttgcctcac ccaagctaga gtgcagtggc ctttgaagct tactacagcc
480
tcaaacttct gggctcaagt gatcctcagc ctcccagtgg tctttgtaga ctgcctgatg
540
gagtctcatg gcacaagaag attaaaacag tgtctccaat tttaataaat ttttgcaatc
600

caaaaaaaaa aaaaaaaaaa aaa
623

<210> 30
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 30
aggagtttct gaggaccatg cac
23

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 31
tcaagggttg gggatacaca cg
22

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer sequence

<400> 32
cttgcttgct ttcttctctg gc
22

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer sequence

<400> 33
agtctggaaa tccacatgac caag
24

<210> 34
<211> 23
<212> DNA
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<220>
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<400> 34
cccaatgagg aacctaaagt tgc
23

<210> 35
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<220>
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<400> 35
ggtgccaaat ctggactctt gtc
23

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 36
gatccatttt cagcagtgct ctg
23

<210> 37
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 37
cagtgttcac agaaggggta ctcac
25

<210> 38
<211> 20
<212> DNA
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<220>
<223> Primer

<400> 38
acgagagcga cacggacaag
20

<210> 39
<211> 20

<212> DNA
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<220>
<223> Primer

<400> 39
tctgaggctg tggcaggtgc
20

<210> 40
<211> 21
<212> DNA
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<220>
<223> Primer

<400> 40
ccagtctttg ccaactcgtg c
21

<210> 41
<211> 23
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<220>
<223> primer sequence

<400> 41
ttcgatcttc aaactgtgcc ttg
23

<210> 42
<211> 20
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<220>
<223> Primer

<400> 42
ttggcaacca gaccagcatc
20

<210> 43
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 43
tttcccatag gtgtgagtgg cg
22

<210> 44
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 44
gactggtgtt ttgttcgggg tc
22

<210> 45
<211> 21
<212> DNA
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<220>
<223> Primer

<400> 45
tttgtccaag gctgcatggt c
21

<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 46
tgccctggtt aagccagaag tc
22

<210> 47
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<400> 47
agcttcactt tggtcttgac gg
22

<210> 48
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<220>
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<400> 48
ggtcatctgc atcaaggttg gc
22

<210> 49
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<220>
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<400> 49
ggttcgtaac cgtgacttca gg
22

<210> 50
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<220>
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<400> 50
gcatcctttt ccagtcttcc g
21

<210> 51
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<220>
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<400> 51
tgcagcaaac atgcctgagc
20

<210> 52
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<220>
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<400> 52
tgttccacga gcaaagcatg tg
22

<210> 53
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<220>
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<400> 53
atccttcttc cactcccgct tc
22

<210> 54
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<220>
<223> Primer

<400> 54
tcggcttgac tacactgtgt gg
22

<210> 55
<211> 22
<212> DNA
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<220>
<223> Primer

<400> 55
tacaaagacc actgggaggc tg
22

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 56
cgggaaatcg tgcgtgacat taag
24

<210> 57
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 57
tgatctcctt ctgcatcctg tcgg
24

<210> 58
<211> 21

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 58
tttggctaca gcaacagggt g
21

<210> 59
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 59
tgtgaggagg ggagattcag tg
22

<210> 60
<211> 16
<212> DNA
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<220>
<223> Primer

<400> 60
cgctgacctc aaccag
16

<210> 61
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 61
ctgtttgccc gttcttatta c
21

<210> 62
<211> 24
<212> DNA
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<220>
<223> Primer

<400> 62
cgggaaatcg tgcgtgacat taag
24

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 63
tgatctcctt ctgcatcctg tcgg
24

<210> 64
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense oligonucleotide

<400> 64
atttgggcat cactggctac aagca
25

<210> 65
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse control oligonucleotide

<400> 65
acgaacatcg gtcactacgg gttta
25

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense oligonucleotide

<400> 66
cagagaggtg agacactcgc cgca
24

<210> 67
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse control oligonucleotide

<400> 67
acgccgctca cagagtggag agac
24

<210> 68
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 68
ttggtgtcat tgggtcaagg gttgg
25

<210> 69
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 69
ggttgggaac tgggttactg tggtt
25

<210> 70
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 70
acagggcaga tacggacctc ggtg
24

<210> 71
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 71
gtggctccag gcatagacgg gaca
24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 72
ttgtgggtaa gcagtttcat gtcgc
25

<210> 73
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 73
cgctgtactt tgacgaatgg gtgtt
25

<210> 74
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 74
cctggatcag acgcaagtta tcggc
25

<210> 75
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 75
cggctattga acgcagacta ggtcc
25

<210> 76
<211> 25
<212> DNA
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